

# Preface

In Volume 1 of “Dynamic Models of Infectious Diseases,” ISBN 978-1-4614-3960-8 and 978-1-4614-3961-5(eBook), we assembled eight chapters from highly acclaimed international scientists who address several of the major insect vector-borne diseases. A diverse and interdisciplinary group of authors was selected with expertise in clinical infectious diseases, epidemiology, molecular biology, human genetics, and mathematical modeling. Indeed, we believe this collection of chapters is unique and should provide a valuable perspective to a wide audience. Though diverse in approach, all the authors address critical elements of disease control. Myriad tools, whether in the realm of molecular engineering, genomic analysis, predictive modeling, or information technology to improve surveillance, are presented in this collection to provide the reader with a current understanding of research methods directed at control of vector-borne diseases.

The present volume is a culmination of a similar effort in the presentation of certain vital non-vector-borne infectious diseases. A variety of intelligent system technology and machine-learning-based methodologies and models have emerged useful in the development of more accurate predictive tools for the early diagnosis of these diseases. There are nine chapters in this book.

Understanding the dynamics of an infectious disease holds the key for designing effective control strategies from a public health perspective. Modeling strategies and effective decision making is the subject of Chap. 1, by V. Sree Hari Rao and M. Naresh Kumar.

This chapter primarily focuses on evolving tools of mathematical modeling as strategies and is generic in nature. Several aspects in the modeling of infectious diseases have been discussed. The authors present new predictive models aimed at better characterization of human susceptibility, disease severity, and control.

Percolation and most epidemics models are concerned with the spatial features of a random subset of some network, with the fundamental difference that while the spread of infectious diseases consists of a dynamical process, the mathematical theory of percolation is concerned with a static random object. In Chap. 2, Alberto Gandolfi has provided a detailed account of the applicability of percolation methods for SEIR epidemic models. This chapter analyzes the role of percolation in

representing or approximating an epidemic model and also discusses the role of percolation in modeling the random networks on which the spread of the infectious diseases takes place.

*Mycobacterium tuberculosis* (*M. tuberculosis*) remains as one of the most dangerous infectious diseases that causes heavy burden on the economy of developing countries and is responsible for more than three million deaths world-wide annually. This is currently considered reemerging and is the subject of discussion in the next three chapters. In Chap. 3, the authors Daniel Okuonghae and Andrei Korobeinikov discuss issues related to the applicability of the WHO-proposed direct observation therapy strategy (DOTS) for the control of this infectious disease with special reference to the developing country Nigeria. This chapter proposes to study the effectiveness of the DOTS strategy through the development of appropriate dynamic mathematical models and also to make practically relevant recommendations for the health authorities.

Classical methods of studying two component systems (TCS) have relied on utilizing biochemical and genetic methods viz. protein characterization and gene inactivation. These methods have been very successful in elucidating the role of various TCSs in bacterial physiology including adaptation to atypical conditions such as pathogenesis. The authors Agrawal, Narayan, and Saini have presented a detailed account of these methodologies in Chap. 4.

Molecular epidemiology tools play an integrative part in tuberculosis control programs in many developed countries at a local and national level. In Chap. 5 Burgos discusses various aspects of *M. tuberculosis*. This chapter presents an overview of the evolution, host–pathogen interactions, and also implications for the control of tuberculosis.

HIV transmission study is the main subject of Chap. 6 by Zhang, Chow, and Wilson. This chapter focusses on knowledge extraction and data modeling based on the trends in HIV transmission according to differences in numbers of sexual partnerships among men who have sex with men in China.

*Cryptococcus gattii* is an emerging infectious disease with an expanding geographic range that gained increased attention in recent years due its frequent outbreaks in North America. This disease is discussed in Chap. 7 by Walraven, Jahng, Davenport, Rane, and Lee. This chapter presents a review on the global and molecular epidemiology, taxonomy, microbial pathogenesis and immunology, and clinical considerations of this emerging fungal pathogen. Further, environmental modeling of the potential ecological niches of *C. gattii* and speculative measures for avoidance and control are discussed.

In Chap. 8, Steinbrück and McHardy discuss the evolutionary dynamics of human viral populations by presenting a technique that leads to the construction of allele dynamics plots (AD-plots) as a method for visualizing the evolutionary dynamics of a gene in a population. The main focus of this chapter rests in the construction of AD-plots for human influenza A viruses such as swine-origin influenza A (H1N1) virus (“swine flu”) and seasonal influenza A (H3N2) virus.

Finally, avian influenza, commonly known as bird flu, is an epidemic caused by H5N1 virus that primarily affects birds such as chickens, wild water birds, ducks,

and swans, and on rare occasions pigs and humans. In recent years this epidemic has emerged as a major global health concern due to its propensity for explosive outbreaks and is the main focus of Chap. 9 by V. Sree Hari Rao and Ranjit Kumar Upadhyay. This chapter aims at developing mathematical models that predict the spread and outbreak diversity of low pathogenic avian influenza virus by presenting a deterministic mathematical model which deals with the dynamics of human infection by avian influenza both in birds and in human, a discrete dynamical model for the spread of H5N1 and the statistical-transmission model of bird flu taking into account the factors that affect the epidemic transmission such as source of infection and social and natural factors.

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